

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 14.7051 Seconds  
(without alignments)  
3334.117 Million cell updates/sec

Title: us-09-972-268-10

Perfect score: 2711  
Sequence: 1 MARIPEPSPLCPGSGKAQIS.....KHNNDPRKAVTDREHYV 510

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

a1 number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %  
Maximum Match 100 %

Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173.5	43.3	407	2 T08732	hypothetical prote
2	565.5	20.9	518	2 JC4024	poliovirus recepto
3	540	19.9	530	2 A53437	poliovirus recepto
4	527	19.4	538	2 I68093	PRR2 delta - human
5	467	17.2	467	1 HLMSP3	poliovirus recepto
6	455	16.8	478	2 I53960	PRR2 alpha - human
7	418	15.4	392	2 B44194	poliovirus recepto
8	418	15.4	417	2 A44194	poliovirus recepto
9	402	14.8	392	1 RMHUPD	poliovirus recepto
10	402	14.8	417	1 RMHUPD	poliovirus recepto
11	326.5	12.0	416	2 A54017	colon carcinoma-as
12	229.5	8.5	764	2 A49448	irregular chlam C
13	204.5	7.5	4391	2 A38096	perlecan precursor
14	196.5	7.2	5175	2 T20992	hypothetical prote
15	196.5	6.9	274	2 T43290	hemichulin precurs
16	187.5	6.7	274	2 A47639	OX-2 membrane glyco
17	181.5	6.7	1896	2 T08851	Down syndrome cell
18	178	6.6	588	2 JH0506	adhesion molecule
19	178	6.6	588	2 A45254	surface glycoprote
20	177.5	6.5	853	1 IUBONC	neural cell adhesi
21	177	6.5	626	1 A61084	myelin-associated
22	177	6.5	637	2 B33785	myelin-associated
23	176	6.5	7962	2 I38346	elastic titin - hu
24	175	6.5	582	1 BNP735	myelin-associated
25	175	6.5	626	1 BNP735	myelin-associated
26	174	6.4	1091	2 A58532	glial cell membran
27	172.5	6.3	3707	2 UC7780	heparan sulfate pr
28	170.5	6.3	365	2 UC7780	coxsackie- and ade
29	164.5	6.1	847	2 JH0371	B-cell adhesion pr

30	162.5	6.0	278	1 TDRTOX	OX-2 membrane glyco
31	162.5	6.0	858	1 IJRTWC	neural cell adhesi
32	162	6.0	587	2 JH0464	DM-GRASP precursor
33	162	6.0	761	1 JH0464	neural cell adhesi
34	162	6.0	765	2 C42632	cell adhesion mole
35	162	6.0	812	2 B42632	cell adhesion mole
36	162	6.0	932	2 A42632	cell adhesion mole
37	161.5	6.0	739	2 JH0581	vascular cell adhe
38	160.5	5.9	702	2 A36319	carcinoembryonic a
39	160	5.9	725	1 JMSNG	neural cell adhesi
40	157	5.8	509	2 J05288	SHP substrate-1 pr
41	157	5.8	1091	1 IJRTWC	neural cell adhesi
42	156	5.8	646	2 I38049	cell surface glyco
43	155	5.7	513	2 J05289	SHP substrate-1 pr
44	154	5.7	1612	2 J30805	ducl1 protein - mo
45	153.5	5.7	1051	2 A39712	kinase-like protei

## ALIGNMENTS

RESULT 1  
T08732  
hypothetical protein DKFZ566B0846.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 11-Jun-1999 #sequence \_revision 11-Jun-1999 #text\_change 13-Aug-1999  
C:Accession: T08732  
R/Ottenswelder, B.; Obermayer, B.; Newes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, May 1999  
A:Reference number: Z16474  
A:Accession: T08732  
A:Molecule type: mRNA  
A:Residues: 1-407 <OTF>  
A:Cross-references: EMBL:AL050071  
A:Experimental source: fetal kidney; clone DKFZ566B0846  
C:Genetics:  
A>Note: DKFZ566B0846.1

Query Match 43.3%; Score 1173.5; DB 2; Length 407;  
Best local similarity 62.8%; Pred. No. 5.8e-79;  
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

QY	143	SGRTYCKAVTPPLNMAOSTTTTTLVETVSLIKGPDSLIDGNETVAALCTAATGKVA	202
DB	1	SGRTYCKAVTPPLNMAOSTTTTTLVETVSLIKGPDSLIDGNETVAALCTAATGKVA	60
QY	203	HI.DWEGD.GEMESITTSFPEYETATIIISQKLFPTFRFARGRITCVVKGHPALBKDIRYSFI	262
DB	61	HI.DWEGD.GEMESITTSFPEYETATIIISQKLFPTFRFARGRITCVVKGHPALBKDIRYSFI	120
QY	263	LIDQYAPVSVTGVGDMVFGKGVNLCNDANPPRFKVSWRIDGMPDGLASDNTL	322
DB	121	LIDQYAPVSVTGVGDMVFGKGVNLCNDANPPRFKVSWRIDGMPDGLASDNTL	180
QY	323	HFVHPLFNTYSGVYICVNTSLGORSQKVIYISDV	359
DB	181	HFVHPLFNTYSGVYICVNTSLGORSQKVIYISDV	240
QY	360	-----FKOTSSINAGVIGAVLAFITAVTVLILPRK--RPSYLDKV	403
DB	241	ERKQAPFLSLATIKDTIATIIASVVGALPIVLSVAGIFPCRRKRTGRGYPKKN	300
QY	404	IDLPTN-----KPPPLTEERSPPLFOKDLFODEH--PLQTOFKEREVG	446
DB	301	Y.IPSIDMQKESQIDVLOODELDPPDSVKKENNPVNNLIRDYIEBPEKTOW-----N	354
QY	447	NLOHNGNLNSRSPYEDENPVG	468
DB	355	NVENNMR--ERPMNDYEDLKG	375

RESULT 2  
JC4024



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## OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 14.7051 Seconds  
(without alignments)  
3354.117 Million cell updates/sec

Title: US-09-972-268-12

Perfect score: 2707

Sequence: 1 MARTLRPSPLCPGGKKAQLS.....KHQNNPKVYIDPREHYV 510

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR\_73:.\*  
2: PIR1:.\*  
3: PIR2:.\*  
4: PIR3:.\*  
5: PIR4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173.5	43.4	407	2 T08732	hypothetical prote
2	565.5	20.9	518	2 JC4024	poliovirus recepto
3	540	19.9	530	2 A53437	poliovirus recepto
4	527	19.5	538	2 I68093	PR2 delta - human
5	467	17.3	467	1 HLMSP3	poliovirus recepto
6	455	16.8	478	2 I53960	PR2 alpha - human
7	418	15.4	392	2 B44194	poliovirus recepto
8	418	15.4	417	2 I44194	poliovirus recepto
9	402	14.9	392	1 RHMUPD	poliovirus recepto
10	402	14.9	392	1 RHMUPD	poliovirus recepto
11	326.5	12.1	416	1 RHMUPD	poliovirus recepto
12	229.5	8.5	764	2 A54017	poliovirus recepto
13	203.5	7.6	4391	2 A54017	colon carcinoma-as
14	196.5	7.3	5198	2 A38096	irregular chiasm C
15	187.5	6.9	274	2 T32992	hemiprecursor
16	187.5	6.7	274	2 T32992	hypothetical prote
17	181.5	6.7	1896	2 T08851	hemiprecursor
18	178.5	6.6	3707	2 JH0506	DX-2 membrane glyco
19	178	6.6	588	2 JH0506	Down syndrome cell
20	178	6.6	588	2 JH0506	heparan sulfate pr
21	177.5	6.6	653	2 A45254	surface glycoprote
22	177	6.5	626	1 A1084	neural cell adhesi
23	177	6.5	637	2 B33785	myelin-associated
24	176	6.5	7962	2 I38346	elastin-associated
25	175	6.5	582	1 BNR13	myelin-associated
26	175	6.5	626	1 BNR13	myelin-associated
27	174	6.4	1091	2 A58532	glial cell membra
28	170.5	6.3	365	2 JC7780	coxsackie- and ade
29	164.5	6.1	847	2 JH0371	B-cell adhesion pr

30	162.5	6.0	278	1 TDRTOX	OX-2 membrane glyco
31	162.5	6.0	858	1 LDRINC	neural cell adhesi
32	162	6.0	587	2 JH0464	DM-GRASP precursor
33	162	6.0	761	1 IJHUNG	neural cell adhesi
34	162	6.0	765	2 C42632	cell adhesion mole
35	162	6.0	812	2 B42632	cell adhesion mole
36	162	6.0	932	2 A42632	cell adhesion mole
37	161.5	6.0	739	2 JN0581	vascular cell adhe
38	160.5	5.9	702	2 A36319	carcinoembryonic a
39	160	5.9	725	1 LUMSG	neural cell adhesi
40	157	5.8	509	2 JC5288	SHP substrate-1 pr
41	157	5.8	1091	1 IJCHNL	neural cell adhesi
42	156	5.8	646	2 I38049	cell surface glyco
43	155	5.7	513	2 JC5289	SHP substrate-1 pr
44	154	5.7	1612	2 T30805	ductal protein - mo
45	153.5	5.7	1051	2 A39712	kinase-like protei

## ALIGNMENTS

## RESULT 1

T08732

hypothetical protein DKFZp566B0846.1 - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999

C/Accession: T08732

R/Ontology: B: Obermaier, B: Mewes, H.W.: Gassenhuber, J.: Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16474

A/Accession: T08732

A/Molecule type: mRNA

A/Residues: 1-407 <OT>

A/Cross-references: EMBL:AL050071

A/Experimental source: fetal kidney; clone DKFZp566B0846

C/Genetics:

A/Notes: DKFZp566B0846.1

## Query Match

43.4% Score 1173.5; DB 2; Length 407;

Best Local Similarity 62.8%; Pred. No. 3.9e-78;

Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

QY	143	SGKTCXAVTPPLGNAGOSTTYYVLYEFTVSLIKGDSLIDGNETVAATCTAATGKPA	202
DB	1	SGKTCXAVTPPLGNAGOSTTYYVLYEFTVSLIKGDSLIDGNETVAATCTAATGKPA	60
QY	203	HTDEGDLGEMESTTTSFPSTATYISQYKLPTRFARGRTICVKKPALEKDIRYSFI	262
DB	61	HTDEGDLGEMESTTTSFPSTATYISQYKLPTRFARGRTICVKKPALEKDIRYSFI	120
QY	263	LDIOYAPRVSUTGVDGWMFVGRKYNLKNADANPPPKSVSRUDGOMPGLASDNTL	322
DB	121	LDIOYAPRVSUTGVDGWMFVGRKYNLKNADANPPPKSVSRUDGOMPGLASDNTL	180
QY	323	HFVHPLTNYSGVITTCVNTSLGQNSDQVYIISDVP-----	359
DB	181	HFVHPLTNYSGVITTCVNTSLGQNSDQVYIISDPTTTLOPTIOMHPSTADIEDAT	240
QY	360	-----FKOTSSIAVAGAVIGAVLAFITAFIVTVLTPRK--RPSYLDKV	403
DB	241	EPKLPPLSTLANTIKODITATYIASVVGALFIVSVLAGIFCYRRARRPRDGYFAKN	300
QY	404	IDLPTP-----KPPVLEERSPLPDKDLFOGHEH--PLQOPPERVYG	446
DB	301	Y-IPPSDMQKESQIDVLAQDQDLPYIPDSYKKNKPNVNLIRKQVLEBPEKTO--N	354
QY	447	NLOHSGINRSRPFYEDENFVG	468
DB	355	NVENLIRP-ERPMDYBDLMKG	375
RESULT 2	JC4024		



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# OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27; Search time 15.6278 Seconds

(without alignments)  
3334.117 Million cell updates/sec

Title: us-09-972-268-2

Perfect score: 2865  
Sequence: 1 SFLPGGKRAQSSASLGLA.....EDDLYSHVDSVSRREMY 542

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Maximum DB seq length: 0,  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2441	74.7	407	2	T08732		Hypothetical prote
2	627	21.9	518	2	JC4024		poliovirus recepto
3	494	17.2	467	1	HLMSP3		poliovirus recepto
4	470	16.4	530	2	A53437		poliovirus recepto
5	463.5	16.2	478	2	I53960		PRR2 alpha - human
6	449.5	15.7	538	2	I68093		PRR2 delta - human
7	422.5	14.7	417	2	A44194		poliovirus recepto
8	415.5	14.5	392	1	B44194		poliovirus recepto
9	390.5	13.6	392	1	RMTUPD		poliovirus recepto
10	390.5	13.6	417	1	RMTUPD		poliovirus recepto
11	331.5	11.6	416	2	A54017		poliovirus recepto
12	230.5	8.0	764	2	A49448		colon carcinoma-as
13	215.5	7.5	4391	2	A38096		irregular chlam C
14	201	7.0	5175	2	T20992		perlecan precursor
15	201	7.0	5198	2	T43290		hypothetical prote
16	198	6.9	588	2	JH0506		hemisciental procu
17	194	6.8	588	2	A45254		adhesin molecule
18	189	6.6	853	1	IJBONC		surface glycoprote
19	187.5	6.5	274	2	A47639		Ox-2 membrane glyci
20	187.5	6.5	7652	2	I38346		elastic titin - hu
21	182	6.4	587	2	JH0464		DM-GRASP precursor
22	181.5	6.3	1896	2	T08851		Down syndrome cell
23	178.5	6.2	847	2	JH0371		B-cell adhesion pr
24	177	6.2	3707	2	S18252		heparan sulfate pr
25	174	6.1	858	1	IJRMNG		neural cell adhesi
26	173.5	6.1	761	1	IJRMNG		neural cell adhesi
27	173	6.0	637	2	B33785		myelin-associated
28	172	6.0	513	2	JCS289		SHP substrate-1 pr
29	171.5	6.0	822	2	B49151		fibroblast growth

30	171	6.0	458	2	S23969		cell-adhesion mole
31	171	6.0	582	1	ENRT35		myelin-associated
32	171	6.0	626	1	ENRT35		myelin-associated
33	171	6.0	1259	2	A43425		Bravo/Mr-CAM cell
34	169.5	5.9	1091	1	IJCHNL		neural cell adhesi
35	169	5.9	626	1	A61084		myelin-associated
36	168	5.9	765	2	C42632		cell adhesion mole
37	168	5.9	812	2	B42632		cell adhesion mole
38	168	5.9	932	2	A42632		cell adhesion mole
39	166.5	5.8	822	2	S19947		fibroblast growth
40	166	5.8	739	2	JN0581		vascular cell adhe
41	165	5.8	725	1	IJMSNL		neural cell adhesi
42	165	5.8	725	1	IJMSNL		neural cell adhesi
43	164.5	5.7	569	2	A46462		T cell activation
44	164	5.7	521	2	JC1508		biliary glycoprote
45	163	5.7	458	1	WMSRL		biliary glycoprote

## ALIGNMENTS

RESULT 1  
T08732  
Hypothetical protein DKFZp566B0846.1 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999-#text\_change 13-Aug-1999  
C/Accession: T08732  
R/Octenvelde, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, May 1999  
A/Reference number: Z16474  
A/Accession: T08732  
A/Molecule type: mRNA  
A/Residues: 1-407<OTF>  
A/Cross-references: EMBL:AL050071  
A/Experimental source: fetal kidney, clone DKFZp566B0846  
A/Genetics:  
A/Note: DKFZp566B0846.1

Query Match 74.7%; Score 2141; DB 2; Length 407;  
Best Local Similarity 99.3%; Pred. No. 3.7e-145;  
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	136	SGKTCATVPPGNAOSTTVTVLEPTSLIKGPDSTLQGNMATAICIAATGKPA	195
DB	1	SGKTCATVPPGNAOSTTVTVLEPTSLIKGPDSTLQGNMATAICIAATGKPA	60
QY	186	HIDWGDGEMESTTSPFNATIIISOYLPTPRPARGRITCVVXHPALEKDIRSFI	255
DB	61	HIDWGDGEMESTTSPFNATIIISOYLPTPRPARGRITCVVXHPALEKDIRSFI	120
QY	256	LDIYAPVAVTGQGNMFVGRKGVNLCNADANPPFKSVWSRLDQMPGLASDNTL	315
DB	121	LDIYAPVAVTGQGNMFVGRKGVNLCNADANPPFKSVWSRLDQMPGLASDNTL	180
QY	316	HPVHPLTFNAGYICKYTNLSIGRSDQKITYISDPPTTTLOPTOMHNSDIEDLAT	375
DB	181	HPVHPLTFNAGYICKYTNLSIGRSDQKITYISDPPTTTLOPTOMHNSDIEDLAT	240
QY	376	EPKCLPPLTLATIKDITATIIASVVGALFTVAVTACIFCYRRRPRGDPYAKX	435
DB	241	EPKCLPPLTLATIKDITATIIASVVGALFTVAVTACIFCYRRRPRGDPYAKX	300
QY	436	YIPSDMOKESQIDVLQODELDYPSVYKKNPNMILRDYIEBEKQNNENINL	495
DB	301	YIPSDMOKESQIDVLQODELDYPSVYKKNPNMILRDYIEBEKQNNENINL	360
QY	496	RFRPMDYEDLNMGRKFSDBHYDENEDLVSHVDSVSRREMY 542	
DB	361	RFRPMDYEDLNMGRKFSDBHYDENEDLVSHVDSVSRREMY 407	

RESULT 2  
JC4024



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## OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 28.4142 Seconds  
(without alignments)  
3930.349 Million cell updates/sec

Title: US-09-972-268-2  
Perfect score: 2866  
Sequence: 1 SPLCPGGGAQSSASASLGA.....ENDIYSHVDSVSRREMY 542

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20604715 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORNITHINE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RECENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAL:\*  
17: SP\_ARCHAEP:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2866	100.0	549	09N083	Q9N863 homo sapien
2	2700	94.2	549	09JL89	Q9J189 mus musculu
3	2656	92.7	549	09D006	Q9D006 mus musculu
4	2341	74.7	407	09Y412	Q9Y412 homo sapien
5	1793.5	62.6	510	09JL87	Q9J187 mus musculu
6	1788.5	62.4	418	09JL87	Q9J187 mus musculu
7	1629	56.8	304	09EVA5	Q9EVA5 homo sapien
8	544	19.0	510	09EVA5	Q9EVA5 homo sapien
9	543	18.9	510	09EVA5	Q9EVA5 homo sapien
10	542	18.9	101	09EVA5	Q9EVA5 homo sapien
11	534.5	18.6	295	09EVA5	Q9EVA5 mesocricet
12	528	18.4	298	09GL74	Q9GL74 ceropithec
13	526.5	18.4	295	09GL75	Q9GL75 bos tauris
14	506	17.7	508	09R007	Q9R007 mus musculu
15	496	17.3	99	09CTR0	Q9CTR0 mus musculu
16	494	17.2	467	09IVT9	Q9IVT9 mus musculu

17	493.5	17.2	463	11	Q9DAP8	Q9DAP8 mus musculu
18	449	15.1	449	4	Q9E16	Q9E16 homo sapien
19	413.5	14.4	412	11	Q9R1E1	Q9R1E1 ratius norv
20	408.5	14.3	412	11	Q9R1E1	Q9R1E1 ratius norv
21	400.5	14.0	401	6	Q9R835	Q9R835 ceropithec
22	393	13.7	408	11	Q9IWP1	Q9IWP1 mus musculu
23	390.5	13.6	417	4	Q9E8J1	Q9E8J1 homo sapien
24	346	12.1	415	11	Q9O977	Q9O977 mus musculu
25	337	11.8	464	11	Q9CRV3	Q9CRV3 mus musculu
26	336.5	11.7	464	11	Q9R5W8	Q9R5W8 mus musculu
27	334.5	11.7	442	4	Q9E167	Q9E167 homo sapien
28	334	11.7	445	11	Q9R4L1	Q9R4L1 mus musculu
29	271.5	9.5	336	11	Q9D6E7	Q9D6E7 mus musculu
30	250	8.7	261	11	Q9D6E7	Q9D6E7 mus musculu
31	247	8.6	396	11	Q9N28	Q9N28 mus musculu
32	234	8.2	959	5	Q9N9Y9	Q9N9Y9 drosophila
33	234	8.2	968	5	Q9N4T9	Q9N4T9 drosophila
34	233	8.1	306	11	Q9OYL4	Q9OYL4 mus musculu
35	233	8.1	432	4	Q9IUP1	Q9IUP1 mus musculu
36	229.5	8.0	975	5	Q9I174	Q9I174 drosophila
37	226.5	7.9	295	11	Q9QYL6	Q9QYL6 mus musculu
38	226.5	7.9	295	11	Q9Z2H8	Q9Z2H8 mus musculu
39	218	7.6	278	11	Q9QYL3	Q9QYL3 mus musculu
40	216	7.5	345	5	Q9W4U1	Q9W4U1 drosophila
41	215.5	7.5	4370	4	Q9H3V5	Q9H3V5 homo sapien
42	212.5	7.4	289	11	Q9QYL5	Q9QYL5 mus musculu
43	209	7.3	388	11	Q9R4E4	Q9R4E4 mus musculu
44	208	7.3	509	11	Q9OWT5	Q9OWT5 ratius norv
45	207	7.2	509	11	P97710	P97710 ratius norv

## ALIGNMENTS

RESULT 1  
Q9N083 PRELIMINARY; PRT; 549 AA.

AC Q9N083: 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Nectin 3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,  
RT Dubreuil P., Lopez M.;  
RT "Human nectin 3/PR3: A novel member of the PVR/PRR/nectin family that  
RT interacts with afadin."  
RL Gene 0:0-0(3200).  
DR EMBL; AF282874; AAP97597.1; -.  
DR InterPro; IPR003599; 1g.  
DR InterPro; IPR003600; 1g\_1like.  
DR InterPro; IPR003606; 1g\_1like.  
DR Pfam; PF00047; 1g; 2.  
DR SMART; SM00409; 1g; 1.  
DR SMART; SM00410; 1g\_1like; 1.  
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CBA9D731 CRC64;

Query Match 100.0%; Score 2866; DB 4; Length 549;  
Best local similarity 100.0%; Pred. No. 4.3e-217;  
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPLCPGGGAQSSASASLGAQLLQPTPTPLLLPLLSRLCGALAGPIVPHVT 60  
DB 8 SPLCPGGGAQSSASASLGAQLLQPTPTPLLLPLLSRLCGALAGPIVPHVT 67  
QY 61 AVMGKNSVSKCIENETTOISWEKHGKSGQTVAVHHPPQYGFSGVGGEGVLFKNTS 120  
DB 68 AVMGKNSVSKCIENETTOISWEKHGKSGQTVAVHHPPQYGFSGVGGEGVLFKNTS 127

QY 121 LNDATITLHNIIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDLSLDGNE 180  
 DB 128 LNDATITLHNIIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDLSLDGNE 187  
 QY 181 TVAAICIAATGKPVAAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFARGRRITCV 240  
 DB 188 TVAAICIAATGKPVAAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFARGRRITCV 247  
 QY 241 VKHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRGKGNLKNADANPPFPKSVMSRL 300  
 DB 248 VKHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRGKGNLKNADANPPFPKSVMSRL 307  
 QY 301 DQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQDQVYISDPPTTTTLOPT 360  
 DB 308 DQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQDQVYISDPPTTTTLOPT 367  
 QY 361 IQWHPSTADIEDLATEPKLPFPLSTLATIKDPTIATIIASVVGALFVLVSVLAGIFC 420  
 DB 428 YRRRTFRGDIYFAKNIIPSDMQESQIDVLQDELSDYPSVKENKNPVNLIKDYL 487  
 QY 481 EPEKTOQNNVENLRFERPMYDIEDLKGMKFPVSDHYDENEDDLVSHVDGVSISRREW 540  
 DB 488 EPEKTOQNNVENLRFERPMYDIEDLKGMKFPVSDHYDENEDDLVSHVDGVSISRREW 547  
 QY 541 YV 542  
 DB 548 YV 549

## RESULT 2

Q9JLB9 ID Q9JLB9 PRELIMINARY, PRT, 549 AA.  
 AC Q9JLB9  
 DT 01-OCT-2000 (TREMELrel. 15, Created)  
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
 DB Cell adhesion molecule nectin-3 alpha.  
 GN PVRL3  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20209403; PubMed=10744716;  
 RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,  
 RA Tachibana K., Mizoguchi A., Takai Y.,  
 RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules  
 RT that shows homophilic and heterophilic cell-cell adhesion  
 RT activities".  
 RL J. Biol. Chem. 275:10291-10299 (2000).  
 DR EMBL; AF195833; AAF63685.1; -.  
 DR MGD; MGI:1930171; Pvr13.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR003600; IG-like.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00409; IG; 1.  
 DR SMART; SM00410; IG-like; 1.  
 SQ SEQUENCE 549 AA; 60583 MW; 5492C9AB8472F195 CRC64;  
 Query Match 94.2%; Score 2700; DB 11; Length 549;  
 Best Local Similarity 93.2%; Pred. No. 5e-204;  
 Matches 505; Conservative 19; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 SPLCPGGKQAQLSSASLGLAGLIQPTPPPLLLLFLPFLLSLGLAGLIIVPEPHT 60  
 DB 8 APICPGGKQAQLSSAFLPAGLLIPAPTPPLLLLFLPFLLSLGLAGLIIVPEPHT 67

QY 61 AVWGKNVSLKCLLEVNETITOLSWEKIHGKSSOTVAHHPOYGFSGVQGRVLPKNYS 120  
 DB 68 AVWGKNVSLKCLLEVNETITOLSWEKIHGKSIQVAHHPOYGFSGVQGRVLPKNYS 127  
 QY 121 LNDATITLHNIIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDLSLDGNE 180  
 DB 128 LNDATITLHNIIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDLSLDGNE 187  
 QY 181 TVAAICIAATGKPVAAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFARGRRITCV 240  
 DB 188 TVAAICIAATGKPVAAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFARGRRITCV 247  
 QY 241 VKHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRGKGNLKNADANPPFPKSVMSRL 300  
 DB 248 VKHPALEKDIRYFILDIOVAPEVSVTGYDGNWFGVGRGKGNLKNADANPPFPKSVMSRL 307  
 QY 301 DQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQDQVYISDPPTTTTLOPT 360  
 DB 308 DQWPDGLLASDNTLHFVHPLTFNYSGVYICKVNSLQORSQDQVYISDPPTTTTLOPT 367  
 QY 361 IQWHPSTADIEDLATEPKLPFPLSTLATIKDPTIATIIASVVGALFVLVSVLAGIFC 420  
 DB 368 YRRRTFRGDIYFAKNIIPSDMQESQIDVLQDELSDYPSVKENKNPVNLIKDYL 487  
 QY 481 EPEKTOQNNVENLRFERPMYDIEDLKGMKFPVSDHYDENEDDLVSHVDGVSISRREW 540  
 DB 488 EPEKTOQNNVENLRFERPMYDIEDLKGMKFPVSDHYDENEDDLVSHVDGVSISRREW 547  
 QY 541 YV 542  
 DB 548 YV 549  
 RESULT 3  
 Q9D006 ID Q9D006 PRELIMINARY, PRT, 549 AA.  
 AC Q9D006  
 DT 01-JUN-2001 (TREMELrel. 17, Created)  
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)  
 DE 2610301B19Rik protein.  
 GN 2610301B19Rik.  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=C57BL/6J; TISSUE=EMBRYO;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Bozell D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.,



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OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 : Search time 12.6003 Seconds

(without alignments)  
3334.117 Million cell updates/sec

Title: US-09-972-268-31

Perfect score: 2299

Sequence: 1 MARTLRSPKCPGCKAQLS.....BRSPPLPKDLFQVCHVEYT 437

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR\_73.\*

1: pirl.\*

2: pirl.\*

3: pirl.\*

4: pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1159.5	50.4	407	2 T08732	hypothetical prote
2	544	23.7	518	2 JC4024	poliovirus recepto
3	495.5	21.6	530	2 A53437	poliovirus recepto
4	490	21.3	538	2 I68093	PR2 delta - human
5	467	20.3	467	1 H1MSJ3	poliovirus recepto
6	455	19.8	478	2 I53960	PKR2 alpha - human
7	418	18.2	392	2 B44194	poliovirus recepto
8	418	18.2	417	2 A44194	poliovirus recepto
9	402	17.5	392	1 RMHUPD	poliovirus recepto
10	402	17.5	417	1 RMHUPD	poliovirus recepto
11	326.5	14.2	416	2 A54017	poliovirus recepto
12	229.5	10.0	764	2 A49448	colicin carcinoma-as
13	205.5	8.9	4391	2 A38096	irregular chlam C
14	196.5	8.5	5175	2 T20992	perlecan precursor
15	196.5	8.5	5198	2 T20992	hemorrhagic prote
16	187.5	8.2	274	2 A47639	Ok-2 membrane glyco
17	178	7.7	588	2 JH0506	adhesion molecule
18	178	7.7	588	2 A45254	surface glycoprote
19	177.5	7.7	853	1 JUBONC	neural cell adhesi
20	177	7.7	626	1 A61084	myelin-associated
21	177	7.7	637	2 -B33785	myelin-associated
22	176	7.7	7962	1 I38346	elastic titin - hu
23	175	7.6	582	1 BNRJ3S	myelin-associated
24	175	7.6	626	1 BNRJ3S	myelin-associated
25	174.5	7.5	1896	2 T08851	Down syndrome cell
26	173.5	7.4	3707	2 S18252	heparin sulfate pr
27	171	7.4	1091	2 A58532	glial cell membran
28	170.5	7.4	365	2 JCT780	coxsackie- and ade
29	164.5	7.2	847	2 JH0371	B-cell adhesion pr

30	162.5	7.1	278	1 TDRTOX	OX-2 membrane glyco
31	162.5	7.1	858	1 J0RTMC	neural cell adhesi
32	162	7.0	587	2 JH0464	DN-GRASP precursor
33	162	7.0	761	1 JH0NG	neural cell adhesi
34	162	7.0	765	2 C42632	cell adhesion mole
35	162	7.0	812	2 B42632	cell adhesion mole
36	162	7.0	932	2 A42632	cell adhesion mole
37	160.5	7.0	702	2 A36319	cardiomyocyte a
38	157	6.8	739	2 JN0381	vascular cell adhe
39	157	6.8	1091	1 J0C8NL	neural cell adhesi
40	156	6.8	646	2 I38049	cell surface glyco
41	154.5	6.7	509	2 J0C5288	SHIP substrate-1 pr
42	154	6.7	1612	2 T30805	ductal protein - mo
43	153.5	6.7	725	1 IJMSNG	neural cell adhesi
44	153.5	6.7	1115	1 IJMSNG	neural cell adhesi
45	153	6.7	1051	2 A39712	kinase-like protei

## ALIGNMENTS

RESULT 1  
T08732  
hypothetical protein DKFZp566B0846.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999  
C:Accession: T08732  
R:Ottensmeyer, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, U.; Wiemann, S.  
Submitted to the Protein Sequence Database, May 1999  
A:Reference number: Z16474  
A:Accession: T08732  
A:Molecule type: mRNA  
A:Residues: 1-407 <OTT>  
A:Cross-references: EMBL:AL050071  
A:Experimental source: fetal kidney; clone DKFZp566B0846  
C:Genetics:  
A:Note: DKFZp566B0846.1

Query Match 50.4% Score 1159.5 DB 2; Length 407;  
Best Local Similarity 70.3% Pred. No. 9.1e-78;  
Matches 230; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

Qy	143	SGKYICAKVTFFPLGNASTVTYVLEPTVSLIKGPSLIDGNETVAIICATGPRVA	202
Db	1	SGKYICAKVTFFPLGNASTVTYVLEPTVSLIKGPSLIDGNETVAIICATGPRVA	60
Qy	203	HTDMSGDMGEMSTTSPFNERTATISQYKLPFRPARGRITCVYKHPALEKDIRYSFI	262
Db	61	HTDMSGDMGEMSTTSPFNERTATISQYKLPFRPARGRITCVYKHPALEKDIRYSFI	120
Qy	263	LDIOYAPREVSVTGDGNMFVGRGVNIKCNADANPPPKSVWSRLDQMPDGLASDNTL	322
Db	121	LDIOYAPREVSVTGDGNMFVGRGVNIKCNADANPPPKSVWSRLDQMPDGLASDNTL	180
Qy	323	HEVHPLEFNTSGVYICKVNTSLGSRSDQKTYISDVP-----	359
Db	181	HEVHPLEFNTSGVYICKVNTSLGSRSDQKTYISDVP-----	240
Qy	360	-----FQTSIVACAVIGAVLAFIIFVVLTPRKK--RPSYLDKV	403
Db	241	EPKLPPLSLATITDDITATIVSVGALFVWSVLAGFCYRRRTFRDYPAR-	299
Qy	404	IDLPTNKPPLVBERSPPLPKDLFQ	430
Db	300	-----NYIPPSDMQKES-----QIDVLQ	317

RESULT 2  
JC4024  
poliovirus receptor-related protein precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 05-Nov-1999  
C:Accession: JC4024



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OM protein - protein search, using SW model

Run on: December 15, 2002, 09:39:57 ; Search time 21 seconds  
(without alignments)  
2513.228 Million cell updates/sec

Title: US-09-972-268-4

Sequence: 2905

Sequence: 1 MARIPEPPLCGGKQQLS.....EDLVSHVDGVSIRREMY 549

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Maximum DB seq length: 0;  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2141	73.7	407	2	T08732
2	627	21.6	518	2	JC4024
3	494	17.0	467	1	HLMSP3
4	470	16.2	530	2	A53437
5	463.5	16.0	478	2	I53960
6	449.5	15.5	538	2	I68093
7	422.5	14.5	417	2	A44194
8	415.5	14.3	392	2	B44194
9	390.5	13.4	392	1	RH01PD
10	390.5	13.4	417	1	RH01PD
11	331.5	11.4	416	2	A54017
12	330.5	7.9	764	2	A49448
13	230.5	7.4	4391	2	A38096
14	201	6.9	5175	2	T20992
15	201	6.9	5198	2	T43290
16	198	6.8	588	2	JH0506
17	194	6.7	588	2	A45254
18	189	6.5	853	1	IJH0NC
19	187.5	6.5	274	2	A47639
20	187.5	6.5	7962	2	I38346
21	182	6.3	587	2	JH0464
22	181.5	6.2	1896	2	T08851
23	179	6.2	3707	2	S18252
24	178.5	6.1	847	2	JH0371
25	174	6.0	858	1	IJH7NC
26	173.5	6.0	761	1	IJH7NC
27	173	6.0	637	1	B31785
28	172	5.9	822	2	JC5289
29	171.5	5.9	822	2	B49151

30	171	5.9	458	2	S23969	cell-adhesion mole
31	171	5.9	582	1	BHRT3	myelin-associated
32	171	5.9	626	1	BHRT3	myelin-associated
33	171	5.9	1259	2	A43425	Bravo/Nr-CAM cell
34	169.5	5.8	1091	1	AI08HL	neural cell adhesi
35	169	5.8	626	1	AI08HL	myelin-associated
36	168	5.8	765	2	C42632	cell adhesion mole
37	168	5.8	812	2	B42632	cell adhesion mole
38	168	5.8	932	2	A42632	cell adhesion mole
39	166.5	5.7	822	2	S19947	fibroblast growth
40	166.5	5.7	822	2	JN0581	vascular cell adhe
41	165	5.7	725	1	IJMSGL	neural cell adhesi
42	165	5.7	1115	1	IJMSGL	neural cell adhesi
43	164.5	5.7	569	2	A46462	cell activation
44	164	5.6	521	2	UC1508	cell activation
45	163	5.6	458	1	WMSK1	cell activation

## ALIGNMENTS

RESULT 1  
T08732  
Hypothetical protein DKF2P566B0846.1 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999  
C/Accession: T08732  
R/Octenwelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, May 1999  
A/Reference number: Z16474  
A/Accession: T08732  
A/Molecule type: mRNA  
A/Residues: 1-407 <OT>  
A/Cross-References: EMBL:AL050071  
A/Experimental source: fetal kidney; clone DKF2P566B0846  
C/Genetics:  
A/Note: DKF2P566B0846.1

Query Match 73.7% Score 2141; DB 2; Length 407;  
Best Local Similarity 99.3%; Pred. No. 3, 7e-145;  
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	143	SGKTCIAVTPPIGNQSTTTVVEPTVSLIKGPSLIDGNETVAICIAATGRVA	202
DB	1	SGKTCIAVTPPIGNQSTTTVVEPTVSLIKGPSLIDGNETVAICIAATGRVA	60
QY	203	HIDWEGDGMSTTSPFNETATIIISQKLPTRFARGRITCVKHPALEKDIRSFI	262
DB	61	HIDWEGDGMSTTSPFNETATIIISQKLPTRFARGRITCVKHPALEKDIRSFI	120
QY	263	LDIQYAEVSVTYDGNWVGRKYNLKCNDANPPPFSSVWSRLDQMPGGLASDNTL	322
DB	121	LDIQYAEVSVTYDGNWVGRKYNLKCNDANPPPFSSVWSRLDQMPGGLASDNTL	180
QY	323	HFVHPLFVNSGYIKVYNSLGSRDQKVIYISDPTTTTLOPTOMHPSTADIEDIAT	382
DB	181	HFVHPLFVNSGYIKVYNSLGSRDQKVIYISDPTTTTLOPTOMHPSTADIEDIAT	240
QY	383	BEKKLPPLSTLTIKDDITATIIISVGGALFVLVSVALGIFCTRRRRFRGGYPAKN	442
DB	241	BEKKLPPLSTLTIKDDITATIIISVGGALFVLVSVALGIFCTRRRRFRGGYPAKN	300
QY	443	VIPPSDMQKSQIDVYQODELSDYPSVYKKNKPVNNIIRNDYEEPEKTOVNVENTN	502
DB	301	VIPPSDMQKSQIDVYQODELSDYPSVYKKNKPVNNIIRNDYEEPEKTOVNVENTN	360
QY	503	REPRMDYEDLQMKKPFVSDHEDYENEDDLVSHVDGSVTSRREMY 549	
DB	361	REPRMDYEDLQMKKPFVSDHEDYENEDDLVSHVDGSVTSRREMY 407	

RESULT 2  
JC4024



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OK protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 14.5321 Seconds

(without alignments)  
3334,117 Million cell updates/sec

Title: US-09-972-268-8

Sequence: 1 PEPDLPQGGKAKQLSSASLIG.....KHQNDPKKVIIDPREHY 504

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: 1: pirl:\*

2: pirl:\*

3: pirl:\*

4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1273.5	43.8	407	2 T08732	hypothetical prote
2	565.5	21.1	518	2 UC4024	poliovirus recepto
3	540	20.2	530	2 A53437	poliovirus recepto
4	527	19.7	538	2 168093	PRR2 delta - human
5	467	17.4	467	1 HLMSP3	poliovirus recepto
6	455	17.0	478	2 153960	PRR2 alpha - human
7	418	15.6	392	2 B44194	poliovirus recepto
8	418	15.6	417	2 A44194	poliovirus recepto
9	402	15.0	392	1 RMRHPD	poliovirus recepto
10	402	15.0	417	1 RMRHPD	poliovirus recepto
11	326.5	12.2	416	2 A54017	poliovirus recepto
12	229.5	8.6	764	2 A49448	colon carcinoma-as
13	204.5	7.6	4391	2 A38096	irregular chlam C
14	196.5	7.3	5175	2 T20992	perlecan precursor
15	196.5	7.3	5198	2 T43290	hypothetical prote
16	187.5	7.0	274	2 A47639	hemiscientin precurs
17	181.5	6.8	1896	2 T08851	OX-2 membrane glyco
18	178	6.6	588	2 JH0506	Down syndrome cell
19	178	6.6	588	2 A45254	adhesion molecule
20	177.5	6.6	853	1 A45254	surface glycoprote
21	177	6.6	626	1 A61084	neural cell adhesi
22	177	6.6	637	1 B33785	myelin-associated
23	176	6.6	7962	2 138346	elastic titin - hu
24	175	6.5	582	1 BNR73S	myelin-associated
25	175	6.5	626	1 BNR73S	myelin-associated
26	174	6.5	1091	2 A58532	glial cell membran
27	170.5	6.4	365	2 J07780	coxsackie- and ade
28	170.5	6.4	3707	2 S18252	heparan sulfate pr
29	164.5	6.1	847	2 JH0371	B-cell adhesion pr

30	162.5	6.1	278	1 TDRTOX	OX-2 membrane glyco
31	162.5	6.1	88B	1 IURTNC	neural cell adhesi
32	162	6.0	587	2 JH0464	DM-GRASP precursor
33	162	6.0	761	1 JH0464	neural cell adhesi
34	162	6.0	765	2 C42632	cell adhesion mole
35	162	6.0	812	2 B42632	cell adhesion mole
36	162	6.0	932	2 A42632	cell adhesion mole
37	161.5	6.0	739	2 J05081	vascular cell adhe
38	160.5	6.0	702	2 A36319	carcinoembryonic a
39	160	6.0	725	1 J05081	neural cell adhesi
40	157	5.9	509	2 J05288	SHP substrate-1 pr
41	157	5.9	1091	1 J05288	neural cell adhesi
42	156	5.8	646	2 I38049	cell surface glyco
43	155	5.8	613	2 J05289	SHP substrate-1 pr
44	154	5.7	1612	2 T30805	ductil protein - mo
45	153.5	5.7	1051	2 A39712	kinase-like protei

#### ALIGNMENTS

##### RESULT 1

T08732  
hypothetical protein DKFZp566B0846.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 11-Jun-1999 #sequence #revision 11-Jun-1999 #text\_change 13-Aug-1999  
C:Accession: T08732  
R:Ottewill, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, May 1999  
A:Reference number: Z16474  
A:Accession: T08732  
A:Molecule type: mRNA  
A:Residues: 1-407 <OTF>  
A:Cross-references: EMBL:AL050071  
A:Experimental source: fetal kidney, clone DKFZp566B0846  
C:Genetics:  
A>Note: DKFZp566B0846.1

Query Match 43.8% Score 1173.5; DB 2; Length 407;

Best Local Similarity 62.8%; Pred. No. 4.5e-78;  
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

Qy	137	SGKYICAVTPPLGNAQSSSTTVTVLEPTVSLIKPDSLLDGNETVAALCIATGKVA	196
Db	1	SGKYICAVTPPLGNAQSSSTTVTVLEPTVSLIKPDSLLDGNETVAALCIATGKVA	60
Qy	197	HIDMEGDLGEMESTTTSFPNETATISQYKLPPTFPAGRRITCVVKKHFALEKDIRYSF1	256
Db	61	HIDMEGDLGEMESTTTSFPNETATISQYKLPPTFPAGRRITCVVKKHFALEKDIRYSF1	120
Qy	257	LDIQYAPRVSSTVDGQWVFGRKGVNLKCNADANPPPKSVMSRLDGMPPDGLASDNTL	316
Db	121	LDIQYAPRVSSTVDGQWVFGRKGVNLKCNADANPPPKSVMSRLDGMPPDGLASDNTL	180
Qy	317	HFVHPPLTNSGVVLCVNTSLGQSDQVLYISDVP-----	353
Db	181	HFVHPPLTNSGVVLCVNTSLGQSDQVLYISDVP-----	240
Qy	354	-----FKOTSSIAAGAVIGAVLALFTIAIVTVLTPRRK--RSPYLDKV	397
Db	241	EPKLPPLSLATLADITATITASVVGALFTIVLSVLAGIFCRRRRRTRGVPAKN	300
Qy	398	IDLPPH-----KPPLYEERSPPPKDLPQEH--PLQTFKREVG	440
Db	301	Y-IIPSDMQKSQIDVLQDELDPYDSVKKENKPNVNLIRDYVABPEKQW-----N	354
Qy	441	NLOHSGNLNRSFEDENPVG	462
Db	355	NVENLNR-ERPMDYEDLMG	375

RESULT 2  
JC4024



Query Match	99.4%; Score 2887; D8 4; Length 549;
Best Local Similarity 99.6%; Pred.No.1.2e-218;	
Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
09N053	
AC 09N053	PRELIMINARY;
AC 09N053	PRT; 549 AA.
DT 01-OCT-2000 (TREMBLrel. 15, Created)	
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE Nectin 3	
OS Homo sapiens (Human)	
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_TaxID=9606;	
RI (1)	
RP SEQUENCE FROM N.A.	
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Piune G.,	
RA Dubreuil P., Lopez M.;	
RT "Human nectin 3/PR3: A novel member of the pVR/PR3/nectin family that	
RT interacts with afadin.;"	
RL Gene 0:0-012000).	
DR EMBL; AF282874; AAF97597.1; -	
DR InterPro; IPR003599; Ig_1.	
DR InterPro; IPR003600; Ig_1like.	
DR InterPro; IPR003006; Ig_MHC.	
DR Pfam; PF00047; Ig_2.	
DR SMART; SM00409; Ig_1.	
DR SMART; SM00410; Ig_1like; 1.	
DR SEQUENCE 549 AA; 61002 MW; 6D104CCBA9D731 CRC64;	
0Y	
0Y 1 MARTGSPPLPGGGRKQLSSASLIGALIGLOPTPLPLILFLPLLSRLGALAPI 60	
Db 1 MARTLRPPLPGGGRKQLSSASLIGALIGLOPTPLPLILFLPLLSRLGALAPI 60	
0Y 61 IYEPHYTVWGNKNSLSKCLIFENYETITQISWEKHGHS SQTAVVHHIPQYGFVSQSYQR 120	
Db 61 IYEPHYTVWGNKNSLSKCLIFENYETITQISWEKHGHS SQTAVVHHIPQYGFVSQSYQR 120	

17	493.5	17.0	449	11	Q9DBP8	Q9DBP8 mus musculus
18	492	14.9	443	1	Q9EBE6	Q9EBE6 homo sapien
19	413.5	14.2	412	11	Q9RIE1	Q9RIE1 ratius norv
20	408.5	14.1	402	11	Q61611	Q61611 ratius norv
21	400.5	13.8	401	6	Q08835	Q08835 ceretopichec
22	393	13.5	408	11	Q91MP1	Q91MP1 mus musculus
23	390.5	13.4	417	4	Q9B8C1	Q9B8C1 homo sapien
24	346	11.9	415	11	Q60377	Q60377 mus musculus
25	337	11.6	404	11	Q9CRV3	Q9CRV3 mus musculus
26	334.5	11.6	456	11	Q9R5M8	Q9R5M8 mus musculus
27	334.5	11.5	442	4	Q98Y67	Q98Y67 homo sapien
28	334	11.5	445	11	Q9R4L1	Q9R4L1 mus musculus
29	271.5	9.3	336	11	Q9DEE7	Q9DEE7 mus musculus
30	250	8.6	361	11	Q9D6A9	Q9D6A9 mus musculus
31	247	8.5	396	11	Q99XZ8	Q99XZ8 mus musculus
32	234	8.1	959	5	Q9N9Y9	Q9N9Y9 mus musculus
33	234	8.1	958	5	Q9M4T9	Q9M4T9 drosophila
34	223	8.0	306	11	Q9O4L4	Q9O4L4 mus musculus
35	223	8.0	432	4	Q9UDE1	Q9UDE1 homo sapien
36	229.5	7.9	975	5	Q97174	Q97174 drosophila
37	226.5	7.8	295	11	Q9OYL6	Q9OYL6 mus musculus
38	226.5	7.8	295	11	Q9Z2H8	Q9Z2H8 mus musculus
39	218	7.5	378	11	Q9OYL3	Q9OYL3 mus musculus
40	216	7.4	345	5	Q9M4U1	Q9M4U1 drosophila
41	215.5	7.4	4370	4	Q9H3V5	Q9H3V5 homo sapien
42	212.5	7.3	289	11	Q9OYL5	Q9OYL5 mus musculus
43	209	7.2	388	11	Q9R164	Q9R164 mus musculus
44	208	7.2	509	11	Q9OW15	Q9OW15 ratius norv
45	207	7.1	509	11	P97710	P97710 ratius norv

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QY 121 VLFRKNSLNDATITLHNIGSDSGKYICKAVTFPLGNAQSSSTTVTLVPTVSLIKGPD 180
DB 121 VLFRKNSLNDATITLHNIGSDSGKYICKAVTFPLGNAQSSSTTVTLVPTVSLIKGPD 180
QY 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPFTR 240
DB 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPFTR 240
QY 241 GRRITCVVKEPALEKDIRSFILDIQYAPEVSVTGYDGNFVGRKGNLKNADANPPP 300
DB 241 GRRITCVVKEPALEKDIRSFILDIQYAPEVSVTGYDGNFVGRKGNLKNADANPPP 300
QY 301 KSVMSRLDGOWPDLGLASNTLHFVHPLTFNYSGVYICKVTNSLQSGQSDQKVIISDPPT 360
DB 301 KSVMSRLDGOWPDLGLASNTLHFVHPLTFNYSGVYICKVTNSLQSGQSDQKVIISDPPT 360
QY 361 TTTLOPTQWHPSTADIEDLATEPKKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
DB 361 TTTLOPTQWHPSTADIEDLATEPKKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDIYPAKNIYIPSDMKESQIDVLQDELDSDYPSVKENKNPVNN 480
DB 421 VLAGIFCYRRRTFRGDIYPAKNIYIPSDMKESQIDVLQDELDSDYPSVKENKNPVNN 480
QY 481 LIRKDYLEEPKQWNNVENLNRPERPMDYEDLQMGKFPVSDHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEEPKQWNNVENLNRPERPMDYEDLQMGKFPVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWTV 549
DB 541 VISRREWTV 549

RESULT 2
Q9JLE9 PRELIMINARY; PRT; 549 AA.
AC Q9JLE9;
AT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DE Cell adhesion molecule nectin-3 alpha.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2029403; PubMed=1074716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizouchi A., Takai Y.
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities."
RL J. Biol. Chem. 275:10291-10299 (2000).
DR EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig_2.
DR SMART; SM00409; IG_1.
DR SMART; SM00410; IG_1like; 1.
SQ SEQUENCE 549 AA; 60583 MW; 549209ABE472F185 CRC64;

Query Match 94.3%; Score 2739; DE 11; Length 549;
Best Local Similarity 93.3%; Pred. No. 5.3e-207;
Matches 512; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 MARTPGSPICPGGGAQSSASLIGACILLOPPTPPPLLLLFLPFLPSRLCALAGPI 60
DB 1 MARTPGSPICPGGGAQSSASLIGACILLOPPTPPPLLLLFLPFLPSRLCALAGSI 60

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QY 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSGQTVAVHHPQYGFVSQGEYQGR 120
DB 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSGQTVAVHHPQYGFVSQGEYQGR 120
QY 121 VLFRKNSLNDATITLHNIGSDSGKYICKAVTFPLGNAQSSSTTVTLVPTVSLIKGPD 180
DB 121 VLFRKNSLNDATITLHNIGSDSGKYICKAVTFPLGNAQSSSTTVTLVPTVSLIKGPD 180
QY 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPFTR 240
DB 181 LIDGNETVAACIAATGKPAHIDWEGDLGEMESTTTSPNETATIIISQYKLPFTR 240
QY 241 GRRITCVVKEPALEKDIRSFILDIQYAPEVSVTGYDGNFVGRKGNLKNADANPPP 300
DB 241 GRRITCVVKEPALEKDIRSFILDIQYAPEVSVTGYDGNFVGRKGNLKNADANPPP 300
QY 301 KSVMSRLDGOWPDLGLASNTLHFVHPLTFNYSGVYICKVTNSLQSGQSDQKVIISDPPT 360
DB 301 KSVMSRLDGOWPDLGLASNTLHFVHPLTFNYSGVYICKVTNSLQSGQSDQKVIISDPPT 360
QY 361 TTTLOPTQWHPSTADIEDLATEPKKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
DB 361 TTTLOPTQWHPSTADIEDLATEPKKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDIYPAKNIYIPSDMKESQIDVLQDELDSDYPSVKENKNPVNN 480
DB 421 VLAGIFCYRRRTFRGDIYPAKNIYIPSDMKESQIDVLQDELDSDYPSVKENKNPVNN 480
QY 481 LIRKDYLEEPKQWNNVENLNRPERPMDYEDLQMGKFPVSDHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEEPKQWNNVENLNRPERPMDYEDLQMGKFPVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWTV 549
DB 541 VISRREWTV 549

RESULT 3
Q9D006 PRELIMINARY; PRT; 549 AA.
AC Q9D006;
AT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE 2610301E19RIK protein.
GN 2610301E19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMERYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Giasi C., King E., Kochiwa H.,
RA Kuehl P., Lewis S., Mateuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtauki S.,
RA Hayashizaki Y.

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